Op

RAW SEQUENCE LISTING   DATE: 09/26/2003
PATENT APPLICATION: **US/10/663,896**   TIME: 09:45:00

Input Set : **N:\Crf3\RULE60\US10663896.raw.txt**
Output Set: **N:\CRF4\09262003\J663896.raw**

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 1 <110> APPLICANT: Reinhard, Christoph
 2 <120> TITLE OF INVENTION: HUMAN CYCLIN-DEPENDANT KINASE (hPNQALRE)
 3 <130> FILE REFERENCE: 200130.459 / 1524.002
 4 <140> CURRENT APPLICATION NUMBER: US/10/663,896
 5 <141> CURRENT FILING DATE: 2003-09-16
 7 <150> PRIOR APPLICATION NUMBER: US/09/464,065
 8 <151> PRIOR FILING DATE: 1999-12-15
10 <160> NUMBER OF SEQ ID NOS: 17
11 <170> SOFTWARE: FastSEQ for Windows Version 4.0
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1002
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapien
17 <400> SEQUENCE: 1
18      ggaccttcta gaatggacca gtactgcatc ctgggccgca tcggggaggg cgcccacggc      60
19      atcgtcttca aggccaagca cgtggagact ggcgagatag ttgccctcaa gaaggtggcc     120
20      ctaaggcggt tggaagacgg cttccctaac caggccctgc gggagattaa ggctctgcag     180
21      gagatggagg acaatcagta tgtggtacaa ctgaaggctg tgttcccaca cggtggaggc     240
22      tttgtgctgg cctttgagtt catgctgtcg gatctggccg aggtggtgcg ccatgcccag     300
23      aggccactag cccaggcaca ggtcaagagc tacctgcaga tgctgctcaa gggtgtcgcc     360
24      ttctgccatg ccaacaacat tgtacatcgg gacctgaaac ctgccaacct gctcatcagc     420
25      gcctcaggcc agctcaagat agcggacttt ggcctggctc gagtcttttc cccagacggc     480
26      agccgcctct acacacacca ggtggccacc aggtctgtgg gctgcatcat gggggagctg     540
27      ttgaatgggt ccccccttt cccgggcaag aacgatattg aacagctttg ctatgtgctt      600
28      cgcatcttgg gcacccccaaa ccctcaagtc tggccggagc tcactgagct gccggactac     660
29      aacaagatct cccttaagga gcaggtgccc atgcccctgg aggaggtgct gcctgacgtc     720
30      tctccccagg cattggatct gctgggtcaa ttccttctct accctcctca ccagcgcatc     780
31      gcagcttcca aggctctcct ccatcagtac ttcttcacag ctcccctgcc tgcccatcca     840
32      tctgagctgc cgattcctca gcgtctaggg ggacctgccc ccaaggccca tccagggccc     900
33      ccccacatcc atgacttcca cgtggaccgg cctcttgagg agtcgctgtt gaacccagag     960
34      ctgattcggc ccttcatcct ggagaggtga ggatcctgag aa                       1002
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 325
38 <212> TYPE: PRT
39 <213> ORGANISM: Homo sapien
40 <400> SEQUENCE: 2
41      Met Asp Gln Tyr Cys Ile Leu Gly Arg Ile Gly Glu Gly Ala His Gly
42       1               5                  10                  15
43      Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val Ala Leu
44                      20                  25                  30
45      Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala
46                      35                  40                  45
47      Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val
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48           50                    55                    60
49      Val Gln Leu Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala
50      65                    70                    75                    80
51      Phe Glu Phe Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln
52                            85                    90                    95
53      Arg Pro Leu Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu
54                    100                   105                   110
55      Lys Gly Val Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu
56            115                   120                   125
57      Lys Pro Ala Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala
58            130                   135                   140
59      Asp Phe Gly Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr
60      145                   150                   155                   160
61      Thr His Gln Val Ala Thr Arg Ser Val Gly Cys Ile Met Gly Glu Leu
62                            165                   170                   175
63      Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu Gln Leu
64                    180                   185                   190
65      Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val Trp Pro
66            195                   200                   205
67      Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile Ser Leu Lys Glu Gln
68            210                   215                   220
69      Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val Ser Pro Gln Ala
70      225                   230                   235                   240
71      Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro His Gln Arg Ile
72                            245                   250                   255
73      Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe Thr Ala Pro Leu
74                    260                   265                   270
75      Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln Arg Leu Gly Gly Pro
76            275                   280                   285
77      Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His Asp Phe His Val
78            290                   295                   300
79      Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu Leu Ile Arg Pro
80      305                   310                   315                   320
81      Phe Ile Leu Glu Arg
82                            325
```

84 <210> SEQ ID NO: 3
85 <211> LENGTH: 1053
86 <212> TYPE: DNA
87 <213> ORGANISM: Homo sapien
88 <400> SEQUENCE: 3
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90      gccaagcacg tggagactgg cgagatagtt gccctcaaga aggtggccct aaggcggttg   120
91      gaagacggct ccctaacca ggccctgcgg gagattaagg ctctgcagga gatggaggac   180
92      aatcagtatg tggtacaact gaaggctgtg ttcccacacg gtggaggctt tgtgctggcc   240
93      tttgagttca tgctgtcgga tctggccgag gtggtgcgcc atgcccagag gccgctagcc   300
94      caggcacagg tcaagagcta cctgcagatg ctgctcaagg gtgtcgcctt ctgccatgcc   360
95      aacaacattg tacatcggga cctgaaacct gccaacctgc tcatcagcgc ctcaggccag   420
96      ctcaagatag cggactttgg cctggctcga gtcttttccc cagacggcag ccgcctctac   480
97      acacaccagg tggccaccag gtggtaccga gcccccgagc tcctgtatgg tgcccgccag   540
```

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98       tatgaccagg gcgtcgatct gtggtctgtg ggctgcatca tggggggagct gttgaatggg   600
99       tccccccttt tcccgggcaa gaacgatatt gaacagcttt gctatgtgct tcgcatcttg   660
100      ggcaccccaa accctcaagt ctggccggag ctcactgagc tgccggacta caacaagatc   720
101      tcctttaagg agcaggtgcc catgcccctg gaggaggtgc tgcctgacgt ctctccccag   780
102      gcattggatc tgctgggtca attccttctc taccctcctc accagcgcat cgcagcttcc   840
103      aaggctctcc tccatcagta cttcttcaca gctcccctgc ctgcccatcc atctgagctg   900
104      ccgattcctc agcgtctagg gggacctgcc cccaaggccc atccagggcc cccccacatc   960
105      catgacttcc acgtggaccg gcctcttgag gagtcgctgt tgaacccaga gctgattcgg  1020
106      cccttcatcc tggaggggtg aggatcctga gaa                                1053
```

108 <210> SEQ ID NO: 4
109 <211> LENGTH: 346
110 <212> TYPE: PRT
111 <213> ORGANISM: Homo sapien
112 <400> SEQUENCE: 4

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113      Met Asp Gln Tyr Cys Ile Leu Gly Arg Ile Gly Glu Gly Ala His Gly
114      1               5                   10                  15
115      Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val Ala Leu
116                      20                  25                  30
117      Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala
118              35                  40                  45
119      Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val
120          50                  55                  60
121      Val Gln Leu Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala
122      65                  70                  75                  80
123      Phe Glu Phe Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln
124                      85                  90                  95
125      Arg Pro Leu Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu
126                      100                 105                 110
127      Lys Gly Val Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu
128              115                 120                 125
129      Lys Pro Ala Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala
130          130                 135                 140
131      Asp Phe Gly Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr
132      145                 150                 155                 160
133      Thr His Gln Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr
134                      165                 170                 175
135      Gly Ala Arg Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys
136                      180                 185                 190
137      Ile Met Gly Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn
138              195                 200                 205
139      Asp Ile Glu Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn
140          210                 215                 220
141      Pro Gln Val Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile
142      225                 230                 235                 240
143      Ser Phe Lys Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp
144                      245                 250                 255
145      Val Ser Pro Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro
146                      260                 265                 270
147      Pro His Gln Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe
```

```
148                275                  280                  285
149      Phe Thr Ala Pro Leu Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln
150          290                  295                  300
151      Arg Leu Gly Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile
152      305                  310                  315                  320
153      His Asp Phe His Val Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro
154                      325                  330                  335
155      Glu Leu Ile Arg Pro Phe Ile Leu Glu Arg
156                      340                  345

158 <210> SEQ ID NO: 5
159 <211> LENGTH: 1092
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapien
162 <400> SEQUENCE: 5
163      atggaccagt actgcatcct gggccgcatc ggggagggcg cccacggcat cgtcttcaag      60
164      gccaagcacg tggagccgag ggtgggctgg cagtgtctgc cttctatcct gcagactggc     120
165      gagatagttg ccctcaagaa ggtggcccta aggcggttgg aagacggctt ccctaaccag     180
166      gccctgcggg agattaaggc tctgcaggag atggaggaca atcagtatgt ggtacaactg     240
167      aaggctgtgt tcccacacgg tggaggcttt gtgctggcct ttgagttcat gctgtcggat     300
168      ctggccgagg tggtgcgcca tgcccagagg ccactagccc aggcacaggt caagagctac     360
169      ctgcagatgc tgctcaaggg tgtcgccttc tgccatgcca acaacattgt acatcgggac     420
170      ctgaaacctg ccaacctgct catcagcgcc tcaggccagc tcaagatagc ggactttggc     480
171      ctggctcgag tctttccccc agacggcagc cgcctctaca cacaccaggt ggccaccagg     540
172      tggtaccgag cccccgagct cctgtatggc gcccgccagt atgaccaggg cgtcgatctg     600
173      tggtctgtgg gctgcatcat gggggagctg ttgaatgggt cccccctttt cccgggcaag     660
174      aacgatattg aacagctttg ctatgtgctt cgcatcttgg gcaccccaaa ccctcaagtc     720
175      tggccggagc tcactgagct gccggactac aacaagatct cctttaagga gcaggtgccc     780
176      atgcccctgg aggaggtgct gcctgacgtc tctccccagg cattggatct gctgggtcaa     840
177      ttccttctct accctcctca ccagcgcatc gcagcttcca aggctctcct ccatcagtac     900
178      ttcttcacag ctccccctgcc tgcccatcca tctgagctgc cggttcctca gcgtctaggg     960
179      ggacctgccc ccaaggccca tccagggccc ccccacatcc atgacttcca cgtggaccgg    1020
180      cctcttgagg agtcgctgtt gaacccagag ctgattcggc ccttcatcct ggaggggtga    1080
181      ggatcctgag aa                                                        1092

183 <210> SEQ ID NO: 6
184 <211> LENGTH: 359
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapien
187 <400> SEQUENCE: 6
188      Met Asp Gln Tyr Cys Ile Leu Gly Arg Ile Gly Glu Gly Ala His Gly
189      1               5                   10                  15
190      Ile Val Phe Lys Ala Lys His Val Glu Pro Arg Val Gly Trp Gln Cys
191                      20                  25                  30
192      Leu Pro Ser Ile Leu Gln Thr Gly Glu Ile Val Ala Leu Lys Lys Val
193                  35                  40                  45
194      Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala Leu Arg Glu
195          50                  55                  60
196      Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val Val Gln Leu
197      65                  70                  75                  80
198      Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala Phe Glu Phe
```

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```
199                       85                    90                    95
200      Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln Arg Pro Leu
201                      100                   105                   110
202      Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu Lys Gly Val
203                      115                   120                   125
204      Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu Lys Pro Ala
205          130                   135                   140
206      Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala Asp Phe Gly
207      145                   150                   155                   160
208      Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr Thr His Gln
209                      165                   170                   175
210      Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr Gly Ala Arg
211                      180                   185                   190
212      Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys Ile Met Gly
213                      195                   200                   205
214      Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu
215          210                   215                   220
216      Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val
217      225                   230                   235                   240
218      Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile Ser Phe Lys
219                      245                   250                   255
220      Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val Ser Pro
221                      260                   265                   270
222      Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro His Gln
223                      275                   280                   285
224      Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe Thr Ala
225          290                   295                   300
226      Pro Leu Pro Ala His Pro Ser Glu Leu Pro Val Pro Gln Arg Leu Gly
227      305                   310                   315                   320
228      Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His Asp Phe
229                      325                   330                   335
230      His Val Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu Leu Ile
231                      340                   345                   350
232      Arg Pro Phe Ile Leu Glu Gly
233                      355
```

235 <210> SEQ ID NO: 7
236 <211> LENGTH: 1038
237 <212> TYPE: DNA
238 <213> ORGANISM: Homo sapien
239 <400> SEQUENCE: 7

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240      atggaccagt actgcatcct gggccgcatc ggggagggcg cccacggcat cgtcttcaag    60
241      gccaagcacg tggagccgag ggtgggctgg cagtgtctgc cttctatcct gcagactggc   120
242      gagatagttg ccctcaagaa ggtggcccta aggcggttgg aggacggctt ccctaaccag   180
243      gccctgcggg agattaaggc tctgcaggag atggaggaca tcagtatgt ggtacaactg    240
244      aaggctgtgt cccacacgg tggaggcttt gtgctggcct ttgagttcat gctgtcggat    300
245      ctggccgagg tggtgcgcca tgcccagagg ccactagccc aggcacaggt caagagctac   360
246      ctgcagatgc tgctcaaggg tgtcgccttc tgccatgcca acaacattgt acatcgggac   420
247      ctgaaacctg ccaacctgct catcagcgcc tcaggccagc tcaagatagc ggactttggc   480
248      ctggctcgag tcttttcccc agacggcagc cgcctctaca cacaccaggt ggccaccagg   540
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